

#2



# ENTERED

OIPE

## RAW SEQUENCE LISTING

DATE: 03/01/2002

PATENT APPLICATION: US/10/073,054

TIME: 10:52:16

Input Set : A:\EP.txt

Output Set: N:\CRF3\03012002\J073054.raw

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3 <110> APPLICANT: Garvan Institute of Medical Research
4   HERZOG, Herbert
6 <120> TITLE OF INVENTION: Novel G-protein coupled receptor-encoding gene and
diagnostic uses
7   therefor
9 <130> FILE REFERENCE: 1871-132 (93702-CIP/MRO)
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/073,054
C--> 11 <141> CURRENT FILING DATE: 2002-02-12
11 <150> PRIOR APPLICATION NUMBER: US 09/308,696
12 <151> PRIOR FILING DATE: 1999-06-11
14 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00805
15 <151> PRIOR FILING DATE: 1998-09-24
17 <150> PRIOR APPLICATION NUMBER: AU P09386
18 <151> PRIOR FILING DATE: 1997-09-24
20 <160> NUMBER OF SEQ ID NOS: 20
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2822
26 <212> TYPE: DNA
27 <213> ORGANISM: Human GPR56-1(TSR32)
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (163)..(2241)
32 <223> OTHER INFORMATION:
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36 cggcagcagg gtctcgctct gtcacacagg ctggagtgcg gtggtgtgat cttggctcat      60
38 cgtaacctcc acctccggg ttcaagtgat tctcatgcct cagcctcccg agtagctggg      120
40 attacaggtg gtgacttcca agagtgactc cgtcggagga aa atg act ccc cag      174
41                                     Met Thr Pro Gln
42                                     1
44 tcg ctg ctg cag acg aca ctg ttc ctg ctg agt ctg ctc ttc ctg gtc      222
45 Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu Leu Phe Leu Val
46 5                               10                               15                               20
48 caa ggt gcc cac ggc agg ggc cac agg gaa gac ttt cgc ttc tgc agc      270
49 Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe Arg Phe Cys Ser
50 25                               30                               35
52 cag cgg aac cag aca cac agg agc agc ctc cac tac aaa ccc aca cca      318
53 Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr Lys Pro Thr Pro
54 40                               45                               50
56 gac ctg cgc atc tcc atc gag aac tcc gaa gag gcc ctc aca gtc cat      366
57 Asp Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu Ala Leu Thr Val His
58 55                               60                               65
60 gcc cct ttc cct gca gcc cac cct gct tcc cga tcc ttc cct gac ccc      414
61 Ala Pro Phe Pro Ala Ala His Pro Ala Ser Arg Ser Phe Pro Asp Pro

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62      70      75      80
64 agg ggc ctc tac cac ttc tgc ctc tac tgg aac cga cat gct ggg aga      462
65 Arg Gly Leu Tyr His Phe Cys Leu Tyr Trp Asn Arg His Ala Gly Arg
66 85      90      95      100
68 tta cat ctt ctc tat ggc aag cgt gac ttc ttg ctg agt gac aaa gcc      510
69 Leu His Leu Leu Tyr Gly Lys Arg Asp Phe Leu Leu Ser Asp Lys Ala
70      105      110      115
72 tct agc ctc ctc tgc ttc cag cac cag gag gag agc ctg gct cag ggc      558
73 Ser Ser Leu Leu Cys Phe Gln His Gln Glu Glu Ser Leu Ala Gln Gly
74      120      125      130
76 ccc ccg ctg tta gcc act tct gtc acc tcc tgg tgg agc cct cag aac      606
77 Pro Pro Leu Ala Thr Ser Val Thr Ser Trp Trp Ser Pro Gln Asn
78      135      140      145
80 atc agc ctg ccc agt gcc gcc agc ttc acc ttc tcc ttc cac agt cct      654
81 Ile Ser Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser Phe His Ser Pro
82      150      155      160
84 ccc cac acg gcc gct cac aat gcc tcg gtg gac atg tgc gag ctc aaa      702
85 Pro His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys
86 165      170      175      180
88 agg gac ctc cag ctg ctc agc cag ttc ctg aag cat ccc cag aag gcc      750
89 Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys Ala
90      185      190      195
92 tca agg agg ccc tcg gct gcc ccc gcc agc cag cag ttg cag agc ctg      798
93 Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln Ser Leu
94      200      205      210
96 gag tcg aaa ctg acc tct gtg aga ttc atg ggg gac atg gtg tcc ttc      846
97 Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met Val Ser Phe
98      215      220      225
100 gag gag gac cgg atc aac gcc acg gta tgg aag ctc cag ccc aca gcc      894
101 Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu Gln Pro Thr Ala
102      230      235      240
104 ggc ctc cag gac ctg cac atc cac tcc cgg cag gag gag gag cag agc      942
105 Gly Leu Gln Asp Leu His Ile His Ser Arg Gln Glu Glu Glu Gln Ser
106 245      250      255      260
108 gag atc atg gag tac tcg gtg ctg ctg cct cga aca ctc ttc cag agg      990
109 Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg Thr Leu Phe Gln Arg
110      265      270      275
112 acg aaa ggc cgg agc ggg gag gct gag aag aga ctc ctc ctg gtg gac      1038
113 Thr Lys Gly Arg Ser Gly Glu Ala Glu Lys Arg Leu Leu Leu Val Asp
114      280      285      290
116 ttc agc agc caa gcc ctg ttc cag gac aag aat tcc agc caa gtc ctg      1086
117 Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn Ser Ser Gln Val Leu
118      295      300      305
120 ggt gag aag gtc ttg ggg att gtg gta cag aac acc aaa gta gcc aac      1134
121 Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn Thr Lys Val Ala Asn
122      310      315      320
124 ctc acg gag ccc gtg gtg ctc act ttc cag cac cag cta cag ccg aag      1182
125 Leu Thr Glu Pro Val Val Leu Thr Phe Gln His Gln Leu Gln Pro Lys
126 325      330      335      340

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128	aat	gtg	act	ctg	caa	tgt	gtg	ttc	tgg	gtt	gaa	gac	ccc	aca	ttg	agc	1230
129	Asn	Val	Thr	Leu	Gln	Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	
130					345					350					355		
132	agc	ccg	ggg	cat	tgg	agc	agt	gct	ggg	tgt	gag	acc	gtc	agg	aga	gaa	1278
133	Ser	Pro	Gly	His	Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	
134					360					365					370		
136	acc	caa	aca	tcc	tgc	ttc	tgc	aac	cac	ttg	acc	tac	ttt	gca	gtg	ctg	1326
137	Thr	Gln	Thr	Ser	Cys	Phe	Cys	Asn	His	Leu	Thr	Tyr	Phe	Ala	Val	Leu	
138					375					380					385		
140	atg	gtc	tcc	tgc	gtg	gag	gtg	gac	gcc	gtg	cac	aag	cac	tac	ctg	agc	1374
141	Met	Val	Ser	Ser	Val	Glu	Val	Asp	Ala	Val	His	Lys	His	Tyr	Leu	Ser	
142					390					395					400		
144	ctc	ctc	tcc	tac	gtg	ggc	tgt	gtc	gtc	tct	gcc	ctg	gcc	tgc	ctt	gtc	1422
145	Leu	Leu	Ser	Tyr	Val	Gly	Cys	Val	Val	Ser	Ala	Leu	Ala	Cys	Leu	Val	
146	405					410					415				420		
148	acc	att	gcc	gcc	tac	ctc	tgc	tcc	agg	gtg	ccc	ctg	ccg	tgc	agg	agg	1470
149	Thr	Ile	Ala	Ala	Tyr	Leu	Cys	Ser	Arg	Val	Pro	Leu	Pro	Cys	Arg	Arg	
150					425					430					435		
152	aaa	cct	cgg	gac	tac	acc	atc	aag	gtg	cac	atg	aac	ctg	ctg	ctg	gcc	1518
153	Lys	Pro	Arg	Asp	Tyr	Thr	Ile	Lys	Val	His	Met	Asn	Leu	Leu	Leu	Ala	
154					440					445					450		
156	gtc	ttc	ctg	ctg	gac	acg	agc	ttc	ctg	ctc	agc	gag	ccg	gtg	gcc	ctg	1566
157	Val	Phe	Leu	Leu	Asp	Thr	Ser	Phe	Leu	Leu	Ser	Glu	Pro	Val	Ala	Leu	
158					455					460					465		
160	aca	ggc	tct	gag	gct	ggc	tgc	cga	gcc	agt	gcc	atc	ttc	ctg	cac	ttc	1614
161	Thr	Gly	Ser	Glu	Ala	Gly	Cys	Arg	Ala	Ser	Ala	Ile	Phe	Leu	His	Phe	
162					470					475					480		
164	tcc	ctg	ctc	acc	tgc	ctt	tcc	tgg	atg	ggc	ctc	gag	ggg	tac	aac	ctc	1662
165	Ser	Leu	Leu	Thr	Cys	Leu	Ser	Trp	Met	Gly	Leu	Glu	Gly	Tyr	Asn	Leu	
166	485					490					495				500		
168	tac	cga	ctc	gtg	gtg	gag	gtc	ttt	ggc	acc	tat	gtc	cct	ggc	tac	cta	1710
169	Tyr	Arg	Leu	Val	Val	Glu	Val	Phe	Gly	Thr	Tyr	Val	Pro	Gly	Tyr	Leu	
170					505					510					515		
172	ctc	aag	ctg	agc	gcc	atg	ggc	tgg	ggc	ttc	ccc	atc	ttt	ctg	gtg	acg	1758
173	Leu	Lys	Leu	Ser	Ala	Met	Gly	Trp	Gly	Phe	Pro	Ile	Phe	Leu	Val	Thr	
174					520					525					530		
176	ctg	gtg	gcc	ctg	gtg	gat	gtg	gac	aac	tat	ggc	ccc	atc	atc	ttg	gct	1806
177	Leu	Val	Ala	Leu	Val	Asp	Val	Asp	Asn	Tyr	Gly	Pro	Ile	Ile	Leu	Ala	
178					535					540					545		
180	gtg	cat	agg	act	cca	gag	ggc	gtc	atc	tac	cct	tcc	atg	tgc	tgg	atc	1854
181	Val	His	Arg	Thr	Pro	Glu	Gly	Val	Ile	Tyr	Pro	Ser	Met	Cys	Trp	Ile	
182					550					555					560		
184	cgg	gac	tcc	ctg	gtc	agc	tac	atc	acc	aac	ctg	ggc	ctc	ttc	agc	ctg	1902
185	Arg	Asp	Ser	Leu	Val	Ser	Tyr	Ile	Thr	Asn	Leu	Gly	Leu	Phe	Ser	Leu	
186	565					570					575				580		
188	gtg	ttt	ctg	ttc	aac	atg	gcc	atg	cta	gcc	acc	atg	gtg	gtg	cag	atc	1950
189	Val	Phe	Leu	Phe	Asn	Met	Ala	Met	Leu	Ala	Thr	Met	Val	Val	Gln	Ile	
190					585					590					595		
192	ctg	cgg	ctg	cgc	ccc	cac	acc	caa	aag	tgg	tca	cat	gtg	ctg	aca	ctg	1998

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193 Leu Arg Leu Arg Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu
194          600          605          610
196 ctg ggc ctc agc ctg gtc ctt ggc ctg ccc tgg gcc ttg atc ttc ttc      2046
197 Leu Gly Leu Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe
198          615          620          625
200 tcc ttt gct tct ggc acc ttc cag ctt gtc gtc ctc tac ctt ttc agc      2094
201 Ser Phe Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser
202          630          635          640
204 atc atc acc tcc ttc caa ggc ttc ctc atc ttc atc tgg tac tgg tcc      2142
205 Ile Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser
206 645          650          655          660
208 atg cgg ctg cag gcc cgg ggt ggc ccc tcc cct ctg aag agc aac tca      2190
209 Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn Ser
210          665          670          675
212 gac tgc gcc agg ctc ccc atc agc tgc ggc agc acc tgc tcc agc cgc      2238
213 Asp Cys Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser Ser Arg
214          680          685          690
216 atc taggcctcca gccacactgc ccatgtgatg aagcagagat gcggcctcgt      2291
217 Ile
220 cgcacactgc ctgtggcccc cgagccaggc ccagccccag gccagtcagc cgcagacttt      2351
222 ggaaagccca acgacatagg agagatgggc cgttgccatg gtggacggac tcccggggct      2411
224 ggggcttttg aattggcctt ggggactact cggctctcac tcagctccca cgggactcag      2471
226 aagtgcgcgc ccatgctgcc tagggtactg tccccacatc tgtcccaacc cagctggagg      2531
228 cctggtctct ccttacaacc cctgggcccc gctcattgc tgggggccag gccttgatc      2591
230 ttgagggtct ggcacatcct taatcctgtg ccctgcctg ggacagaaat gtggctccag      2651
232 ttgctctgtc tctcgtggtc accctgaggg cactctgcat cctctgtcat tttaacctca      2711
234 ggtggcacc agggcgaaatg gggcccaggg cagaccttca gggccagagc cctggcggag      2771
236 gagaggccct ttgccaggag cacagcagca gctcgcctac ctctgagccc g      2822
239 <210> SEQ ID NO: 2
240 <211> LENGTH: 693
241 <212> TYPE: PRT
242 <213> ORGANISM: Human GPR56-1(TSR32)
244 <400> SEQUENCE: 2
246 Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu
247 1          5          10          15
250 Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe
251          20          25          30
254 Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr
255          35          40          45
258 Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu Ala
259          50          55          60
262 Leu Thr Val His Ala Pro Phe Pro Ala Ala His Pro Ala Ser Arg Ser
263 65          70          75          80
266 Phe Pro Asp Pro Arg Gly Leu Tyr His Phe Cys Leu Tyr Trp Asn Arg
267          85          90          95
270 His Ala Gly Arg Leu His Leu Leu Tyr Gly Lys Arg Asp Phe Leu Leu
271          100          105          110
274 Ser Asp Lys Ala Ser Ser Leu Leu Cys Phe Gln His Gln Glu Glu Ser
275          115          120          125

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278 Leu Ala Gln Gly Pro Pro Leu Leu Ala Thr Ser Val Thr Ser Trp Trp
279      130      135      140
282 Ser Pro Gln Asn Ile Ser Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser
283 145      150      155      160
286 Phe His Ser Pro Pro His Thr Ala Ala His Asn Ala Ser Val Asp Met
287      165      170      175
290 Cys Glu Leu Lys Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His
291      180      185      190
294 Pro Gln Lys Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln
295      195      200      205
298 Leu Gln Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp
299      210      215      220
302 Met Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu
303 225      230      235      240
306 Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln Glu
307      245      250      255
310 Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro Arg Thr
311      260      265      270
314 Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu Lys Arg Leu
315      275      280      285
318 Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln Asp Lys Asn Ser
319      290      295      300
322 Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile Val Val Gln Asn Thr
323 305      310      315      320
326 Lys Val Ala Asn Leu Thr Glu Pro Val Val Leu Thr Phe Gln His Gln
327      325      330      335
330 Leu Gln Pro Lys Asn Val Thr Leu Gln Cys Val Phe Trp Val Glu Asp
331      340      345      350
334 Pro Thr Leu Ser Ser Pro Gly His Trp Ser Ser Ala Gly Cys Glu Thr
335      355      360      365
338 Val Arg Arg Glu Thr Gln Thr Ser Cys Phe Cys Asn His Leu Thr Tyr
339      370      375      380
342 Phe Ala Val Leu Met Val Ser Ser Val Glu Val Asp Ala Val His Lys
343 385      390      395      400
346 His Tyr Leu Ser Leu Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu
347      405      410      415
350 Ala Cys Leu Val Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu
351      420      425      430
354 Pro Cys Arg Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn
355      435      440      445
358 Leu Leu Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu
359      450      455      460
362 Pro Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile
363 465      470      475      480
366 Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu Glu
367      485      490      495
370 Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr Tyr Val
371      500      505      510
374 Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly Phe Pro Ile

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date